

**Amendments to the Claims:**

The listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-31 - cancelled

32. (previously presented) A method of detecting the silencing of a target gene in an organism, wherein said silencing is initiated by introduction of an exogenous nucleic acid, which method comprises the steps of:

- (i) obtaining a sample of material from said organism,
- (ii) producing a nucleic acid extract from said sample,
- (iii) analyzing said extract such as to determine the presence or absence of short RNA molecules which are 21-25 nucleotides in length (SRMs) in said extract,
- (iv) characterizing any SRMs which are present in said extract such as to determine sequence identity or similarity with said target gene, and
- (v) correlating the presence of said SRMs having sequence identity or similarity with said target gene in the extract with the occurrence of gene silencing in said organism.

33. (previously presented) A method in accordance with claim 32, wherein the organism is a plant.

34. (previously presented) A method in accordance with claim 32, wherein the organism is a nematode.

35. (previously presented) A method in accordance with claim 32, wherein the organism is a mammal.

36.. (previously presented) A method in accordance with claim 32 wherein the SRMs are short anti-sense RNA molecules (SARMs).

37. (previously presented) A method in accordance with claim 32 wherein the SRMs are short sense RNA molecules (SSRMs).

38. (previously presented) A method in accordance with claim 32, wherein the gene silencing is post-transcriptional gene silencing (PTGS).

39. (previously presented) A method in accordance with claim 32, wherein the silencing of said target gene in the organism is associated with pathogen derived resistance.

40. (previously presented) A method in accordance with claim 32, wherein the silencing of said target gene in the organism is associated with modification of a specific trait by co-suppression of the target gene.

41. (previously presented) A method of identifying a silenced target gene in an organism in which gene silencing is detected as claimed in claim 32, which method further comprises the steps of:

- (vi) preparing a library of genes from said organism, and
- (vii) identifying those genes in said library which share sequence identity or similarity, with any SRMs which are present in the extract as being genes which are silenced in the organism.

42. (previously presented) A process for isolating one or more RNA molecules associated with target gene silencing from a sample of material from an organism, wherein the RNA molecules are SRMs which share sequence identity with the target gene, and wherein said silencing is initiated by introduction of an exogenous nucleic acid, which process comprises the steps of:

- (a) producing a nucleic acid extract from said sample,

(b) purifying said extract to produce purified RNA molecules which are 21-25 nucleotides in length by carrying out at least one purification step selected from the following steps (i) filtration; (ii) differential precipitation (iii) ion exchange chromatography, such as to isolate said SRMs.

43. (previously presented) A process according to claim 42 which further comprises the step of separating the purified RNA molecules according to size by electrophoresis through a gel, which gel is a 15% polyacrylamide gel containing 7M urea as a denaturant and TBE (0.5x) as a buffer.

44. (previously presented) A process according to claim 43 which further comprises the step of transferring the RNA molecules on the gel to a hybridization membrane by electrophoresis.

45. (previously presented) A process according to claim 44 which further comprises the step of labeling RNA molecules on the hybridization membrane using a radioactive probe obtained from a single stranded RNA molecule transcribed in vitro from a plasmid DNA template.

46. (previously presented) A process for isolating a silencing agent comprising SRMs for a target gene from an organism, which process comprises the steps of:

- (i) silencing said target gene in said organism, wherein said silencing is initiated by introduction of an exogenous nucleic acid,
- (ii) obtaining a sample of material from said organism,
- (iii) performing a process in accordance with claim 42 to isolate said SRMs.

47. (previously presented) A method according to claim 32 wherein the target gene is an animal gene selected from the group consisting of: a gene involved in apoptosis; a gene involved in cell-cycle regulation; and a gene involved in a neurological process.

48. (previously presented) A method as claimed in claim 32, wherein said short RNA molecules are between 23 and 25 nucleotides in length.

49. (previously presented) A method as claimed in claim 32, wherein said short RNA molecules are 25 nucleotides in length.

50. (New) A method of determining the identity of a gene the translation of which in a cell is undergoing post-transcriptional gene silencing, which method comprises the steps of:

- (i) obtaining sample material from said cell;
- (ii) producing a nucleic acid extract from said sample;
- (iii) analyzing said extract such as to determine the presence or absence of short RNA molecules which are 25 nucleotides in length plus or minus 1, 2, 3, 4 or 5 nucleotides (SRMs) in said extract;
- (iv) characterizing any SRMs which are present in said extract to determine the nucleotide sequence of said SRMs; and
- (v) utilizing the sequences of said SRMs to screen a genomic or cDNA library of said cell to thereby ascertain the identity of any genes the translation of which in said cell is undergoing post-transcriptional gene silencing.

51. (New) The method of Claim 50 wherein said cell is derived from a plant, a mammal, an insect, an avian organism, a reptile, a protozoan or nematode.

52. (New) The method of Claim 51 wherein said cell is derived from a plant.

53. (New) The method of Claim 51 wherein said cell is derived from a mammal.

54. (New) The method of Claim 53 wherein said cell is derived from a rodent.

55. (New) The method of claim 51 wherein said SRMs comprise sense and antisense RNA molecules complementary to a gene in said cell.

56. (New) The method of claim 55 wherein said sense and antisense RNA molecules are present in essentially equimolar amounts.

57. (New) A method for determining the pathogen derived resistance status in a plant which comprises:

(i) obtaining a sample of said plant; and

(ii) quantifying SRMs present in said sample of said plant for content of SRMs having sequence homology to sequences present in a pathogen, the pathogen derived resistance to which is sought to be determined for said plant.

58. (New) The method of Claim 57 wherein said plant is selected from the group consisting of cereal plants, crop plants, and horticultural plants.

59. (New) The method of Claim 57 wherein the plant is selected from maize, wheat, potato, tapioca, rice, sorghum, millet, cassava, barley, pea, oilseed rape, sugar beet, sunflower, soybean, lettuce, endive, cabbage, broccoli, cauliflower,

carnation, geranium, tobacco, cucurbits, carrot, strawberry, tomato, pepper, chrysanthemum, poplar, eucalyptus, and pine.

60. (New) The method of claim 57 wherein said SRMs comprise sense and antisense RNA molecules.

61. (New) The method of claim 60 herein said sense and antisense RNA molecules are present in essentially equimolar amounts.

62. (New) A method for identifying or characterizing temporal gene translational effects in an organism which comprises.

(i) obtaining samples of said organism at different times;

(ii) quantifying SRMs present in said samples of said organism for content of SRMs;

(iii) identifying genes having sequence homology to SRMs found in said samples to vary in amount with respect to the selected times at which the sample was obtained.

63. (New) The method of Claim 62 wherein said organism is selected from the group consisting of a plant, a mammal, an avian organism, an insect, a reptile, a nematode and a protozoan.

64. (New) The method of claim 62 wherein said SRMs comprise sense and antisense RNA molecules complementary to a gene in said organism.

65. (New) The method of claim 64 wherein said SRMs are present in essentially equimolar amounts.